

Gencore version 4.5
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OM protein - protein search, using sw model.

Run on: March 1, 2001, 16:16:33 ; Search time 91.75 Seconds
(without alignments)
234.418 Million cell updates/sec

Title: US-09-331-631a-3

Sequence: 3532 MAINTNSLCSLFLSFLU.....SSRSYKQQQPLVSILDFVGF 666

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1092	30.9	605	1 VCLA_GOSHI	P09799 gossypium h
2	1083.5	30.7	588	1 VCLA_GOSHI	P09801 gossypium h
3	899	25.5	573	1 VHL_ARAIV	P15590 zea mays (m
4	873.5	24.7	614	1 AHL_ARAIV	P43237 arachis hyp
5	872.5	24.7	639	1 GCK_XOEN	P18187 glycine max
6	865.5	24.5	626	1 AHL_ARAIV	P43238 arachis hyp
7	855.5	24.2	605	1 GLC_SOYEN	P13916 glycine max
8	832.5	23.6	571	1 CVC_APEA	P13915 pisum sativ
9	798	22.6	524	1 SBP_SOYBN	Q04672 glycine max
10	760.5	21.5	459	1 VCLC_PEA	P13918 pisum sativ
11	748	21.2	439	1 GLCB_SOYEN	P25974 glycine max
12	711.5	20.1	463	1 VCLL_VICFA	P08438 vicia faba
13	704.5	19.9	410	1 VCLB_PEA	P02854 pisum sativ
14	689.5	19.5	445	1 CANA_CANEN	P50477 canavalia e
15	682.5	19.3	445	1 CANA_CANGL	P05629 canavalia g
16	568	16.1	436	1 PHSB_HAVU	KW FT SIGNAL 1 23
17	557	15.8	421	1 CVCL_PEA	FT CHAIN 24 605 KW SIGNAL 1 23
18	499.5	14.1	386	1 VCLB_PEA	SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC64;
19	414	11.7	275	1 TRYHUMAN	
20	226	6.4	1998	1 TRYHUMAN	
21	22	6.3	1407	1 TRYRABBIT	
22	203	5.7	1549	1 TRY_SHEEP	
23	190.5	5.4	124	1 VCELL_BEA	
24	185	5.2	499	1 GLUZ_ORYSA	
25	180.5	5.1	500	1 GLUZ_ORYSA	
26	180.5	5.1	544	1 INVO_AOPTR	
27	180.5	5.1	1033	1 GLP_DROME	
28	178	5.0	499	1 GLUB_ORYSA	
29	178	5.0	1391	1 MST2_DROHY	
30	177.5	5.0	471	1 RUL1_XENOPUS	
31	175	5.0	1085	1 YARA_SCIPHO	
32	174.5	4.9	887	1 YLX8_CABEL	
33	171	4.8	1 LPGL_EMETME		

RESULT	4			
AH11_ARAHY		STANDARD;	PRT;	614 AA.
ID	AH11_ARAHY			
AC	PA3237;			
PA3237;				
DT	01-NOV-1995 (Rel. 32, created)			
01-NOV-1995 (Rel. 32, last sequence update)				
DT	01-NOV-1997 (Rel. 35, last annotation update)			
DT	01-NOV-1997 (Rel. 35, last annotation update)			
DE	ALLERGEN Ara H 1, CLONE p17 (ARA H 1).			
OS	Arachis hypogaea (Peanut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Arachis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV: FLORRUNNER;			
RX	MEDLINE:96013631; Pubmed=7560062;			
RA	Burks A.W., Cockrell G., Stanley J.S., Helm R.M., Bannon G.A.;			
RT	"Recombinant Peanut allergen Ara h 1 expression and IgE binding in patients with peanut hypersensitivity.";			
RL	J. Clin. Invest. 96:1715-1721(1995).			
R1	-i - SIMILARITY: TO 7S SERED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCNIN, ETC.).			
CC	-----			
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CC	-----			
CC	EMBL: L38853; AAA0336.1; -.			
DR	RSP; PS0477; ICAW.			
DR	INTERPRO: IPR01113; -.			
DR	PFAM: PF00546; Seedstore_7s; 1.			
KW	Allergen.			
SQ	SEQUENCE 614 AA; 70283 MW; 1DDACF217EEC5F31 CRC64;			
Query Match	24.7%	Score 873.5; DB 1; Length 614;		
Best Local Similarity	34.3%	Pred. No. 7.7e47;		
Matches	208;	Conservative 115; Mismatches 205; Indels 79; Gaps 16;		
QY	102 CQPRCKECEGEEEYNRQDPQQYEQCCERCQRETERPHMQTCQQRCCR - VKEKR 159			
Db	36 CAQRCLOSQCQEPPDLKQ ----- ACESRCTKLEYDPRCVYDVTCATNRHPPGERTRG 88			
QY	160 KOKKRYEQSQREDEEKYERMEKEDNK - - RDPOOREYEDCRRRCQEQQPRQYCQCR C 216			
Db	89 ROPGDDYDDDRRORP-----REGGGRWGPAPRERERE-----DWROPREWD--RRP 133			
QY	217 REQ-----RQHGRGGDLNIPQRGSGSRVYEPEEEKOSDNIPYFDEDSLSTRFRTECHISV 272			
Db	134 SHOQPKRIRPREGGE-----QEGTPYPSVCRETSRNPRPSRFESTYQNGRIVR 189			
QY	273 LENFYGRSKKLRAKKNYRIVLLEAQNPNATWLPHLDATLTLVGGRALKMIHRDNE 332			
Db	190 LORFDQRSKQFQNQHRIVOERAPNTLVLPKHADADNLVIQOGQATTVANGNIRK 249			
QY	333 YNLECGDVTRIPAGTTFYLINRDRNERLIAKEIQLTISPQYKEFPAGQNPPEPLST 392			
Db	250 FNLDGEHALLRIPSGFISYLNRHDNQNLWAKISMVPNTPGOFEDPPASSRDSQSYLG 309			
QY	393 FSKEIIEALANTIOAERLJGVL-----GQQR----- EGVLISASQEIREL 432			
Db	310 FRNTTAAFAFNNEFLYRVEENAGGEEERSRRSTRSSDNEQGVYKVSKELWFL 369			

DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	ALLERGEN ARA H 1, CLONE P41B (ARA H T).
OS	Arachis hypogaea (Peanut).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
OC	Fabales; Fabaceae; Papilionoideae; Arachis.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SRRN-CV: FLORUNNER;
RX	MEDLINE:96013631; PubMed:7560062;
RA	Burks A. W., Cockrell G., Stanley J.S., Helm R.M., Bannon G.A.;
RT	"Recombinant peanut allergen Ara h 1 expression and IgE binding in patients with peanut hypersensitivity.";
RL	J. Clin. Invest. 96(7):1715-1721(1995)
CC	-!- SIMILARITY: TO 75 SEED STORAGE PROTEINS (PHASEOLIN, VICTILIN, CONVICTILIN, CONGLYCIINT, ETC.).
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CC	-----
CC	EMBL; L34402; ARB00861.1; ~.
DR	HSSP; P50477; ICAM.
DR	INTERPRO; IPR001113; ~.
DR	PFAM; PF00546; Seedstore_7s; 1.
KW	Allergen.
SEQUENCE	626 AA; 71345 MW; 1A6BBB4149D0E3 CRC64;
Query Match	24.5%; Score 865.5; DB 1; Length 626; Best Local Similarity 34.7%; Pred. No. 2.5e-46; Matches 213; Conservative 105; Mismatches 209; Indels 87; Gaps 18;
Q93	ESGPRDQQY--CQRCKEICIEEEYENRQRDPQQYEQOCERCQRHETEPR-----H 142
: : : : : : : :	-----
D26	KSSPYQKRTENPCACQRLCQSQQEPDDLLQK-----ACESRCTKLEYDPRCVDPGRH 78
Q94	143 MOTCQQR--ERR-----YEKKRKQQRYYEQOREDEEKYERMKEDDNKRDPQQR 192
:	-----
D79	TGTNTNQRSPGPGRTRGQPGDYDDRR-QPREEGGRGAGPGREREED-WRQPR-- 133
Q95	193 EYEDCRRCEQQEPRQYQCORRCRQECORQHQRGGRGLINPORGGSRYEEGEEKSDNPY 252
:	-----
D134	--EDWRAPSHQO-PR-----KIRPECREGE---QEWGFGSHUREETSNNPF 175
Q96	253 YFDERSLSTRFRTEEGHISVLNFYGRSKLRLAKNYRLVILEANPAFLVPLTHADAI 312
:	-----
D176	176 YFPSSRFSTTRYGNQNGLRVLQRFDRDSRFOFLNQHTRIVOLEAKPNTLVLPKHADNT 235
Q97	313 LIVGGGALKMHRDNRSENLCECGDVIRPAGFTYLINRDNNEHLHAKFLQTISTP 372
:	-----
D236	236 LVIQSOATVTANGNRKSENPLDEHALRIPSGFTSYLNRHDQNLRYKATPSVNTP 295
Q98	373 GOYKEFFPAGGONPEVPLSTSKEELALNTOAQERIGVL-----GOOR-- 417
:	-----
D296	296 QOFDEDFPASSRQDSOYLOGSRSRNTEAFAWAFFNETRRVLEENAGGEQBERGORRWST 355
Q99	418 -----EGVITASASQIRELTDSESRRWRHTRGGECSRQ---PYNLFNKRPLYSNK 467
:	-----
D356	356 RSSENNENBEGVIVKVKSEHEVEELTKHAKS----VSKKSEEEGDTINPINLREGEPDLSSN 410
Q100	468 YGQAYEVKEPEYR-QLOMDMYSVFIANITQCSMMGPPFN'RSTKAVVVASGEADEMACP 526
:	-----
D411	411 FGKLFKEVKPDKNPQDLMCLTCVKEGALMLPHFNSKAMVTVVNKGTLGNEELVALV 470
Q101	527 HLGSGRHGRGKRRHEREEDV---HYEVALRSREATVVPVGHVVVFVSSGMNLL 582
D471	471 REQOQRGRBEEDEDEEGSNREVRYTARLKEGVFTMPAHVAINASSHLI- 529
Query Match	24.2%; Score 855.5; DB 1; Length 605; Best Local Similarity 31.4%; Pred. No. 9.8e-46; Matches 194; Conservative 143; Mismatches 211; Indels 69; Gaps 15;
Q102	72 YDNQDDPQTDCQOCORCROOESPRQQVCQRC-----KEICEEEE--EYNQRDP 122
Db	1 : :: :
Db	27 YWEKENPKHN--KCLOCNSRDSYRNAQ-CHARENLKVKEECEGEJPRPRPQHP 83
Q103	123 QOQEYOQCOERQRHETPRIMOTCQRCRERYEKEKQORRYYEQQREDEEKYERMK 182
Db	84 FREPQPQGEKEDEDQEPRPPIPFRPQPROFEEHEOREEOWPKEEKRGKSEEDED 143

RN :|||
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
 RC TISSUE-EMBRYO;
 RX MEDLINE=93104680; PubMed=1467654;
 RA Gimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D.;
 RT "A 62-kD sucrose binding protein is expressed and localized in
 tissues actively engaged in sucrose transport.";
 RL Plant Cell 4:1561-1574(1992).
 CC -!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -!- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
 SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
 MESOPHYLL CELLS OF YOUNG STINK LEAVES, THE COMPANION CELLS OF
 MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
 CC -!- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
 CC UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
 FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
 DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
 EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
 RATE OF SUCROSE UPTAKE IN THE COTYLEDON.

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CC EMBL: L06388; AAB03894.1; -.
 CC DR PIR: J01730; J01730.
 CC DR INTERPRO: IPR001113; -.
 CC DR PFAM: PF00346; Seedstore_7s; 1.
 KW FT SIGNAL_1; 29
 FT CHAIN_30; 524 AA; 60522 MW; 0251EE90796EF341 CRC64;
 SQ

Query Match 22.6%; Score 798; DB 1; Length 524;
 Best Local Similarity 33.2%; Pred. No. 2; 9e-42;
 Matches 190; Conservative 100; Mismatches 180; Indels 102; Gaps 16;
 CC Qy 105 RCKEICEEEEYENQRDPQ--QQYEQOCQERQRHETEPHMOTCOCORCERYEKRRKQQ 162
 Db 27 KCKETEVVEE-----DPELVCKHQCCQQQYTCGDKR--VCLQSCD-RYHRKQRE 76
 CC Qy 163 KRYEQEQREDKEVKYERMKNECDNKRDPPQREYEDCCRRCBQEPPRQQYDCORRCFQQQ 222
 Db 77 KQIOETTREKKEE-ESEREE-----EQEQ 101
 CC Qy 223 HGRGGIGLINPQRGGSQSERVEECEKQSDNPYFDE RSLSTRFRTRTEGHISVLENYGRSK 281
 Db 102 H-----EDDENPYIIFEDDKDFETRVETRVEFGIRIVLKFFTESK 140
 CC Qy 282 LLRLAKNYRLVLEAPNAFVLPHTHDADALLVTFGRGALKMIRDNRNSYLNLCGDIV 341
 Db 141 LLOGTENFLAILEPRAHTAEVSPRFDESEVVFNTKGAVLGLVSESETKITLEPGDMI 200
 CC Qy 342 RIPAGTMYFLINRDNNEHLHA-KFLQTISTPGQKREFPAGGNPEPLSTREKIE 399
 Db 201 HIPAGPGLPVLNDRENDKLFAMLHPVSVTPGKFEEFPAGGDPEPSLAFSAFWNLQ 260
 CC Qy 400 AALNTQTAERLKGVLGSGOREGTVTISASOEORELTDUDSEERRWHTRGGSSRGHYNLEN 459
 Db 261 ALQQTPIRKGLENVFDQNEGSIFRISREQVHALA-PTKKSSWWPP--GGE-SKPOFNIFS 316
 CC Qy 460 KRPLPSNPKYQGAYVERPEDIYQ-LODMDSVFINITOQSMMGPFNFTRSTKVWVASG 517
 Db 317 KRPTLSNGYGLTEVGPDDDEKSWLQLMLTFTNTOSMSMTHYNSHATKIALVLD 376
 CC Qy 518 EADVEMACPHLSGRGRRGGKRHEEEDVHYEQKARLSKREAIVWPVGHVVVSSGN 577

RESULT 10
 VCLC_PEA STANDARD; PRT; 459 AA.
 AC P13916;
 ID 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VICILIN PRECURSOR.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytas;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Pisum.
 CC [1] SEQUENCE FROM N.A.
 RC Higgins T.J.V., Newbiggin E.J., Spencer D., Llewellyn D.J., Craig S.;
 RA "The sequence of a pea vicilin gene and its expression in transgenic
 tobacco.";
 RL Plant Mol. Biol. 11:683-695(1988).
 RN [2]
 RN SEQUENCE OF 27-459 FROM N.A. (CLONE PDUB9).
 RC STRAIN=CV; FELTHAM FIRST;
 RX MEDLINE=88326226; PubMed=3046604;
 RA Watson M.D., Lambert N., Delaunay A., Yarwood J.N., Croy R.R.D.,
 RA Gatehouse J.A., Wright D.J., Boulter D.;
 RT "Isolation and expression of a pea vicilin cDNA in the yeast
 Saccharomyces cerevisiae.";
 RL Biochem. J. 251:857-864(1988).
 CC -!- FUNCTION: SEED STORAGE PROTEIN.
 CC -!- SUBCELLULAR LOCATION: COTYLEDONYAR MEMBRANE-BOUND VACUOLAR PROTEIN
 CC BODIES.
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 11 GENES FOR VICILIN SUBUNITS.
 CC -!- SIMILARITY: TO OTHER TS SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
 CC CONVICILIN, CONGLYCIIN, ETC.)
 CC ---
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 CC ---
 CC EMBL; X14076; CAA32239.1;
 DR EMBL; Y00722; CAA68108.1; -.
 DR PIR; S00567; S00567.
 DR PIR; S08505; S08505.
 DR HSSP; P50477; ICAW.
 DR INTERPRO; IPR001113; -.
 DR PF00546; Seedstore_7s; 1.
 DR KW Seed storage protein; Multigene family; Signal.
 FT SIGNAL_1; 28
 FT CHAIN_29; 459
 FT VICILIN.
 FT CONFLICT 375 375
 FT CONFLICT 409 409 I -> V (IN REF. 2).
 FT SEQUENCE 459 AA; 52231 MW; E2FA390B95451D29 CRC64;

Query Match 21.5%; Score 760.5; DB 1; Length 459;
 Best Local Similarity 37.6%; Pred. No. 5e-40;
 Matches 161; Conservative 79; Mismatches 159; Indels 29; Gaps 5;

ID	VCLB-PEA	PRT;	410 AA.
AC	P02854;	STANDARD;	
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	01-JAN-1990 (Rel. 13, Last annotation update)		
DE	PROVICILIN PRECURSOR (TYPE B) (FRAGMENT).		
OS	<i>Pisum sativum</i> (Garden pea).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids I; OC Fabales; Fabaceae; Papilionoideae; <i>Pisum</i> .		
RN	[1]		
RP	SEQUENCE FROM N A. (CLONES PDBB7 AND PDBA4).		
RC	STRAIN=CV. FELTHAM FIRST;		
RX	MEDLINE=83220791; PUBMED=6687941;		
RA	Lycett G. W., Delaunay A. J., Gatehouse J. A., Gilroy J., Croy R. R. D., RA Boulier D.;		
RA	"The vicilin gene of pea (<i>Pisum sativum</i> L.): a complete cDNA coding sequence for preprovicilin";		
RL	Nucleic Acids Res. 11:2367-2380(1983).		
CC	-!- FUNCTION: SEED STORAGE PROTEIN.		
CC	-!- SUBCELLULAR LOCATION: COLEOPTILE MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.		
CC	-!- SIMILARITY: TO OTHER TS SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCIININ, ETC.).		
CC	PIR: A03344; FWPMB.		
DR	HSSP: P50477; ICMW.		
DR	INTERPRO: IPR00113; -.		
DR	PFAM: PF00546; Seedstore_7s; 1.		
KW	Seed storage protein; Glycoprotein; Multigene family; Signal.		
FT	SIGNAL 1 15		
FT	CHAIN 16 >410 PROVICILIN.		
FT	SITE 221 222 CLEAVAGE (POTENTIAL).		
FT	CARRIER 250 350 >500 (C-terminal).		

RESULT 13

CANA_CANEN
ID CANA CANEN
STANDARD:
PRT: 445 AA

AC P50477; DT 01-OCT-1996 (Rel. 34, Created) DT 01-OCT-1996 (Rel. 34, Last sequence update) DE CANAVALIN PRECURSOR OS Canavalia ensiformis (Jack bean) (Horse bean). OC Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; OC Fabaceae; Papilionoideae; Canavalia. RN [1] SEQUENCE FROM N.A. RC TISSUE=COPTILEDON; RX MEDLINE=92119225; PubMed=1731957; RA Ng J.D., Stinchcombe T., Ko T.-P., Alexander E., McPherson A.; RT "PCR cloning of the full-length cDNA for the seed protein canavalin from the jack bean plant," *Canavalia ensiformis.*"; RL *Plant Mol. Biol.* 18:147-149(1992). RN [2] SEQUENCE FROM N.A. RC TISSUE=COPTILEDON; RX MEDLINE=94143475; PubMed=8310055; RA Ng J.D., Ko T.-P., McPherson A.; RT "Cloning, expression and crystallization of jack bean (*Canavalia ensiformis*) canavalin"; RL *Plant Physiol.* 101:713-728(1993). RN [3] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS). RX MEDLINE=94143476; PubMed=8310056; RA Ko T.-P., Ng J.D., McPherson A.; RT "The three dimensional structure of canavalin from jack bean (*Canavalia ensiformis*)."; RL *Plant Physiol.* 101:729-744(1993). CC -!- FUNCTION: SEED STORAGE PROTEIN. CC -!- SUBUNIT: HOMOTIMER. CC -!- SIMILARITY: TO OTHER TS SEED STORAGE PROTEINS (PHASEOGLIN, VICILIN, CONVICILIN, CONGIGCININ, ETC.). CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). CC CC EMBL; X59467; CAA42075.1; - . DR PDB; ICAU; 31-OCT-93. DR PDB; ICAX; 31-OCT-93. DR PDB; ICW; 31-OCT-93. DR PDB; ICX; 31-OCT-93. DR INTERPRO; IPR001113; -. DR PFAM; PF00546; Seedstore_7s; 1. KW Seed storage protein; Signal; 3D-structure. FT SIGNAL 1 26 FT CHAIN 27 445 AA; SEQUENCE 445 AA; MW: 30383C5FB3A1E9B7 CRC64;

Query Match 19.5%; Score 689.5; DB 1; Length 445; Best Local Similarity 33.6%; Pred. No. 1.1e-35; Matches 143; Conservative 97; Mismatches 163; Indels 23; Gaps 5;

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QY 414 GQOREGVVISHASQEIQIRELARDDESRRWIIIRGGESSRGPFYLNKRPLXSNKYQAYE 473 DR 212 QEEQEGVIVKPKDQIQEISHTQAQSSSRKTF--SSQDPRFENLSRDPYTSNNYKLYE 267 DR 474 VPKPEDYHQLOQMDVSFIANTTQGSMGPFRTRSPTKVVVVAASGERADVENACPHLSGRIG 533 DR : ||| ::||| : ::||| : | | | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| 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QY 414 GQOREGVVISHASQEIQIRELARDDESRRWIIIRGGESSRGPFYLNKRPLXSNKYQAYE 473 DR 212 QEEQEGVIVKPKDQIQEISHTQAQSSRKTF--SSQDPRFENLSRDPYTSNNYKLYE 267 DR 474 VPKPEDYHQLOQMDVSFIANTTQGSMGPFRTRSPTKVVVVAASGERADVENACPHLSGRIG 533 DR : ||| ::||| : ::||| : | | | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

QY 591 MNHENFLAGRNVNLOQIEPAMELAFAAPRKEVELNSQDESIFPPGPRRHOQSSRS 650 DR 268 TPEKNSQLRQDILLNCLQNMEGALFVPHNSRATVLSIVTSSPVALKAASDLNNV--GIGVNAE 318 DR 534 GRRGGRKHEEEDVHVEOKV--ARLSKREAVIVPGHPVSGNENULLFAFGINAQ 590 DR 319 ---GIEQQQQGLESMOLRYAATSEGDIIVTSSPVALKAASDLNNV--GIGVNAE 372 DR 373 NNERNFLLAGHENVIRQIPROVSIDLTPGSGCEEVELENQKESVFDQPRIDAGKA 432 DR QY 651 TRQQQP 656 DR 433 RRAHLP 438

Db RESULT 15 ID CANA_CANGL STANDARD: PRT; 445 AA. AC P10562; DR 01-JUL-1989 (Rel. 11, Created) DT 01-JUL-1989 (Rel. 11, Last sequence update) DE CANAVALIN PRECURSOR. OS Canavalia gladiata (Japanese jack bean). CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; OC Fabaceae; Papilionoideae; Canavalia. RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 27-40. DR TISSUE=SEED; RX MEDLINE=8811636; PubMed=3338449; RA Yamauchi D., Nakamura K., Asahi T., Minamikawa T.; RT cDNAs for canavalin and concanavalin A from *Canavalia gladiata* seeds. Nucleotide sequence of cDNA for RNA from canavalin A mRNAs in developing seeds.; RL Eur. J. Biochem. 170:515-520(1988). DR INTERPRO; IPR001113; -. DR PFAM; PF00546; Seedstore_7s; 1. KW Seed storage protein; Signal; 3D-structure. FT SIGNAL 1 26 FT CHAIN 27 445 AA; SEQUENCE 445 AA; MW: 30383C5FB3A1E9B7 CRC64;

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FT	CONFLICT	161	161	N -> K (IN REF. 2).	DB 1;	Length 445;
SQ	SEQUENCE	445 AA;	50289 MW;	739B59CCC2292EA80	CRC64;	
Query	Match	19.3%	Score 682.5;	DB 1;	Length 445;	
Best Local Similarity	33.1%	Pred. No. 3e-35;	Mismatches	164;	Indels 23;	Gaps 5;
Matches	141;	Conservative	98;			
QY	235	GGSGRYEEGEEKQSDNPYFDERSLSTPRTEEGHSIVLENFYGRSLLRATKNYRLLVLL	294			
Db	32	GGEDDESEESRSQQNPNFLFRSNKFLFKNQHGLRLQRENEDTEKLENRDYRLEY	91			
QY	295	EANNAFAVLPHTHDADATILVNGRGALKMTHDRNRSYNLUCCGDVWRTPAQTYLNR	354			
Db	92	CSKRNTLLPHHSDSLVLVLEGQAILVLVNPDDGTYKLDQDAIKIQAGTPFYLNP	151			
QY	355	DNNERLHAKELOTLISPGQYKEFPAGGQNPEPYLSKILEALNTQERL RGVL	413			
Db	152	DNNQNLRLINFAITFRRIPTVEDFLUSTKRPLSYLASFKNFLFEASYDSPYDEI BOTLL	211			
QY	414	QQOREGVITASOQIRELTRODDESRWRWHIRRGESSRGPVNLFNRPLYSNKKYSONYE	473			
Db	212	QESEGIVVKMPKDQIQLISKHAQSSRKTL---SSQDKPENLRSRDPIVSNNGLYE	267			
QY	474	VKFEDYRQLQMDVSFLANTQVQSMGPFENRSTKVWVVAASGEAVEMACPHLSGRHG	533			
Db	268	IPPEKNSQLRDLIDILLNCLQMNEGALEFVPHYNRSRATVILVANEGRAVELV-----	318			
QY	534	GRKGKKRHEEEEDVHYEQK--ARLSKREAIVPVGHFWFVSSGNENULLAFGINAQ	590			
Db	319	---GLEOOQQQGLESMOLRRYAAUTSEGDLIVIPSSFPVALKAASDLNMV--GIGVNAE	372			
QY	591	NNHENFLAGRNVNLOQTEPQAMELAFAAPRKEVEELFNSODESITFPGPROHQOQSRS	650			
Db	373	NNERFLAGNKENVIROIPROVSDLITFGSGBEVEELLENQKESYFVDGQFRHIDGGKA	432			
QY	651	TROOP 656				
Db	433	RRAHLP 438				

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 Job time: 417 sec

